

Abstract of the Disclosure

Methods for determining transcription rate of mRNA in eukaryotic cells using nuclear runoff transcription where labeled RNA molecules are hybridized against an array of at least 500 nucleic acid molecule probes representing at least part of the genome of the native eukaryotic organism to identify the quantity of nascent mRNA transcripts in said cells. The method can be used to simultaneously identify the quantity of a large number of mRNA transcripts. A rate of degradation for distinct mRNA in a eukaryotic cell rate is determined by comparing a steady state mRNA with nuclear runoff mRNA. Steady state to nuclear runoff ratios are used to determine gene and mRNA structure function relations that leads to gene expression and mRNA stability, predict structural determinants for mRNA stability and predict regulatory motifs for transcription rates. Methods of constructing recombinant organisms with enhanced stability for mRNA expressed from a gene of interest comprise introducing into the genome of an organism a gene containing one or more sequence elements that confer structural stability on mRNA transcribed from said gene.